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<110> Commonwealth Scientific and Industrial Research
Organisation

<120> Modified Proteins

<130> A-70233/RFT

<140> PCT/AU99/00563

<141> 1999-07-12

<150> AU PP4604

<151> 1998-08-10

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09/743533-4004

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<400> 13
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<210> 14
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<400> 14
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 cttgcagcgt cccccaacaa gcttcatgca tatggagtat ggtctaggga tccgggtacc 120
 gagctcgaat tcgccctata 140

<210> 15

<211> 20

<212> PRT

<213> Artificial Sequence

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<223> unknown

<400> 15

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1				5					10					15	
Trp	Ser	Met	Val												
			20												

<210> 16

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> unknown

<400> 16

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ccagtgcctg	tgccagcggc	catagcccta	gcgctaattg	cagcaggctt	tgtcacgtca	180
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<210> 17

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<212> PRT

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<223> unknown

<400> 17

Gln Ala Leu Lys Ala Ala Thr Ala Thr Ala Ala Gly Ser Leu Leu Val
 1 5 10 15
 Leu Ser Gly Leu Ile Leu Ala Gly Thr Val Ile Ala Leu Thr Val Ala
 20 25 30
 Thr Pro Val Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Ala Ile
 35 40 45
 Ala Leu Ala Leu Met Ser Ala Gly Phe Val Thr Ser Gly Gly Leu Gly
 50 55 60
 Val Ala Ala Leu Ser Ser Phe Ser Val Leu Ala Asn Thr Ala Cys Ile
 65 70 75 80
 Trp

<210> 18

<211> 477

<212> DNA

<213> Artificial Sequence

<220>

<223> unknown

<400> 18

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 cacacacccc aacaatattt cccctatcta ccagaggaat tgtttcccca atatcaaata 180
 ccaaccccc tacaaccaca acaaccattc cccaacaac cacaacaacc tcttcctcgg 240
 cccaacaac cattcccctg gcaaccacaa caaccatttc ccagccccca agaaccaatt 300
 cccaacaac cattcccctg gcaaccacaa caaccatttc ccagccccca agaaccaatt 360
 caacaaataa ttttccagca accccaacaa tcataccctg tgcaacctca acagccattt 420
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<211> 158

<212> PRT

<213> Artificial Sequence

<220>

<223> unknown

<400> 19

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      20              25              30
Pro Phe Pro Val Gln Gln Pro Phe His Thr Pro Gln Gln Tyr Phe Pro
      35              40              45
Tyr Leu Pro Glu Glu Leu Phe Pro Gln Tyr Gln Ile Pro Thr Pro Leu
      50              55              60
Gln Pro Gln Gln Pro Phe Pro Gln Gln Pro Gln Gln Pro Leu Pro Arg
65              70              75              80
Pro Gln Gln Pro Phe Pro Trp Gln Pro Gln Gln Pro Phe Pro Gln Pro
      85              90              95
Gln Glu Pro Ile Pro Gln Gln Pro Gln Gln Pro Phe Pro Gln Gln Pro
      100             105             110
Gln Gln Pro Phe Pro Gln Gln Pro Gln Gln Ile Ile Phe Gln Gln Pro
      115             120             125
Gln Gln Ser Tyr Pro Val Gln Pro Gln Gln Pro Phe Pro Gln Gln Pro
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Gln Pro Val Pro Gln Gln Ala Ser Cys Ile Trp Ser Met Val
145             150             155

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<210> 20

<211> 338

<212> DNA

<213> *Aspergillus niger*

<400> 20

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acggcatagc tctgagtgct gacaagtaca cttccagcga cccgctctgg tatgtcactg 180
tgactctgcc ggctggtgag tcgtttgagt acaagtttat ccgcattgag agcgatgact 240

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ccgtggagtg ggagagtgat cccaaccgag aatacacctg tcctcaggcg tgcggaacgt 300
cgaccgcgac ggtgactgac acctggcggg gcatatgg 338

<210> 21

<211> 112

<212> PRT

<213> Aspergillus niger

<400> 21

Ala	Ser	Thr	Thr	Pro	Thr	Ala	Val	Ala	Val	Thr	Phe	Asp	Leu	Thr	Ala
1				5				10					15		
Thr	Thr	Thr	Tyr	Gly	Glu	Asn	Ile	Tyr	Leu	Val	Gly	Ser	Ile	Ser	Gln
			20				25						30		
Leu	Gly	Asp	Trp	Glu	Thr	Ser	Asp	Gly	Ile	Ala	Leu	Ser	Ala	Asp	Lys
	35						40					45			
Tyr	Thr	Ser	Ser	Asp	Pro	Leu	Trp	Tyr	Val	Thr	Val	Thr	Leu	Pro	Ala
	50					55					60				
Gly	Glu	Ser	Phe	Glu	Tyr	Lys	Phe	Ile	Arg	Ile	Glu	Ser	Asp	Asp	Ser
65					70				75					80	
Val	Glu	Trp	Glu	Ser	Asp	Pro	Asn	Arg	Glu	Tyr	Thr	Val	Pro	Gln	Ala
				85				90					95		
Cys	Gly	Thr	Ser	Thr	Ala	Thr	Val	Thr	Asp	Thr	Trp	Arg	Cys	Ile	Trp
			100				105						110		

<210> 22

<211> 371

<212> DNA

<213> Artificial Sequence

<220>

<223> unknown

<400> 22

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tcgccaagca gcagtgtgtg ggggagcttg caaacattcc gcagcagtgc cgatgccagg 180

cgctgcgcta cttcatgggg ccgaagtctc gtccggatca gagcggcctc atggaactcc 240
 ccggatgccc tagggaggtg cagatggact tcgtgaggat actcgtcacg ccgggggtact 300
 gcaacttgac gaccgttcac aacactccgt actgcctcgc tatggaggag tctcagtgga 360
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<210> 23

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> unknown

<400> 23

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Pro	Leu	Pro	Ser	Cys	Arg	Asp	Tyr	Val	Glu	Gln	Gln	Ala	Cys	Arg	Ile
			20					25						30	
Glu	Thr	Pro	Gly	Ser	Pro	Tyr	Leu	Ala	Lys	Gln	Gln	Cys	Cys	Gly	Glu
			35					40						45	
Leu	Ala	Asn	Ile	Pro	Gln	Gln	Cys	Arg	Cys	Gln	Ala	Leu	Arg	Tyr	Phe
			50				55					60			
Met	Gly	Pro	Lys	Ser	Arg	Pro	Asp	Gln	Ser	Gly	Leu	Met	Glu	Leu	Pro
65					70					75				80	
Gly	Cys	Pro	Arg	Glu	Val	Gln	Met	Asp	Phe	Val	Arg	Ile	Leu	Val	Thr
					85					90				95	
Pro	Gly	Tyr	Cys	Asn	Leu	Thr	Thr	Val	His	Asn	Thr	Pro	Tyr	Cys	Leu
					100					105				110	
Ala	Met	Glu	Glu	Ser	Gln	Trp	Ser	Cys	Ile	Trp					
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<210> 24

<211> 123

<212> PRT

<213> Artificial Sequence

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<223> unknown

<400> 24

Ala Ile Gly Asn Glu Asp Cys Thr Pro Trp Thr Ser Thr Leu Ile Thr
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 20 25 30
 Glu Met Pro Gly Pro Pro Tyr Leu Ala Lys Gln Glu Cys Cys Glu Gln
 35 40 45
 Leu Ala Asn Ile Pro Gln Gln Cys Arg Cys Gln Ala Leu Arg Tyr Phe
 50 55 60
 Met Gly Pro Lys Ser Arg Pro Asp Gln Ser Gly Leu Met Glu Leu Pro
 65 70 75 80
 Gly Cys Pro Arg Glu Val Gln Met Asn Phe Val Pro Ile Leu Val Thr
 85 90 95
 Pro Gly Tyr Cys Asn Leu Thr Thr Val His Asn Thr Pro Tyr Cys Leu
 100 105 110
 Gly Met Glu Glu Ser Gln Trp Ser Cys Ile Trp
 115 120

<210> 25

<211> 377

<212> DNA

<213> wheat

<400> 25

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 ggcgttggtg gaaatggtgg aaggagggtt gtcaagagct ccttggggag tgttgagtc 180
 ggctcggcca aatgccaccg caatgccgct gcaacatcat ccaggggtca atccaaggcg 240
 atctcgggtg catcttcgga tttcagcgtg atcgggcaag caaagtata caagaagcca 300
 agaacctgcc gccaggtgc aaccagggcc ctccctgcaa catccccggc actattggct 360
 attactggtg catatgg 377

<400> 26

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Thr	Lys	Leu	Asn	Ser	Cys	Arg	Asn	Tyr	Leu	Leu	Asp	Arg	Cys	Ser	Thr
			20					25					30		
Met	Lys	Asp	Phe	Pro	Val	Thr	Trp	Arg	Trp	Trp	Lys	Trp	Trp	Lys	Gly
		35					40					45			
Gly	Cys	Gln	Glu	Leu	Leu	Gly	Glu	Cys	Cys	Ser	Arg	Leu	Gly	Gln	Met
	50					55					60				
Pro	Pro	Gln	Cys	Arg	Cys	Asn	Ile	Ile	Gln	Gly	Ser	Ile	Gln	Gly	Asp
65					70					75					80
Leu	Gly	Gly	Ile	Phe	Gly	Phe	Gln	Arg	Asp	Arg	Ala	Ser	Lys	Val	Ile
				85					90					95	
Gln	Glu	Ala	Lys	Asn	Leu	Pro	Pro	Arg	Cys	Asn	Gln	Gly	Pro	Pro	Cys
			100					105					110		
Asn	Ile	Pro	Gly	Thr	Ile	Gly	Tyr	Tyr	Trp	Cys	Ile	Trp			
		115					120					125			